

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/500,912  
Source: PT  
Date Processed by STIC: 12-14-04

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 12/14/2004

PATENT APPLICATION: US/10/500,912

TIME: 10:40:33

Input Set : A:\X-14934.ST25.txt

Output Set: N:\CRF4\12102004\J500912.raw

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3 <110> APPLICANT: Burris, Thomas P.
5 <120> TITLE OF INVENTION: Method of Treating Atherosclerosis and Hypercholesterolemia
7 <130> FILE REFERENCE: X-14934
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/500,912
C--> 9 <141> CURRENT FILING DATE: 2004-07-08
9 <160> NUMBER OF SEQ ID NOS: 10
11 <170> SOFTWARE: PatentIn version 3.3
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 1528
15 <212> TYPE: DNA
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23 gcagccaggc ccagggaggc agcagctgca tcctcagaga ggaagccagg atgccccact      180
25 ctgctggggg tactgcaggg gtggggctgg aggctgcaga gccacagacc ctgctcacca      240
27 gggcagagcc cccttcagaa cccacagaga tccgtccaca aaagcggaaa aaggggccag      300
29 cccccaaaat gctggggaac gagctatgca gcgtgtgtgg ggacaaggcc tcgggcttcc      360
31 actacaatgt tctgagctgc gagggctgca agggattctt ccgccgcagc gtcatacaagg      420
33 gagcgcacta catctgccac agtggcggcc actgccccat ggacacctac atgcgtcgca      480
35 agtgccagga gtgtcggtct cgcaaagcc gtcaggctgg catgcgggag gagtgtgtcc      540
37 tgtcagaaga acagatccgc ctgaagaaac tgaagcggca agaggaggaa caggctcatg      600
39 ccacatcctt gccccccagg cgttcctcac cccccaaaat cctgccccag ctccagcccgg      660
41 aacaactggg catgatcgag aagctcgtcg ctgccagca acagtgtaac cggcgctcct      720
43 tttctgaccg gcttcgagtc acgccttggc ccatggcacc agatccccat agccgggagg      780
45 cccgtcagca gcgctttgcc cacttcaactg agctggccat cgtctctgtg caggagatag      840
47 ttgactttgc taaacagcta cccggcttcc tgcagctcag ccgggaggac cagattgccc      900
49 tgctgaagac ctctgcgac gaggtgatgc ttctggagac atctcggagg tacaacctg      960
51 ggagtgaag tatcaccttc ctcaaggatt tcagttataa ccgggaagac tttgccaaag     1020
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61 tgaaactggg gagcctccgg accctgagca gcgtccactc agagcaagtg tttgcaactgc     1320
63 gtctgcagga caaaaagctc ccaccgctgc tctctgagat ctgggatgtg cacgaatgac     1380
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72 <210> SEQ ID NO: 2
73 <211> LENGTH: 447
74 <212> TYPE: PRT
75 <213> ORGANISM: homo sapiens
77 <400> SEQUENCE: 2

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84 20 25 30
87 Gln Gly Gly Ser Ser Cys Ile Leu Arg Glu Glu Ala Arg Met Pro His
88 35 40 45
91 Ser Ala Gly Gly Thr Ala Gly Val Gly Leu Glu Ala Ala Glu Pro Thr
92 50 55 60
95 Ala Leu Leu Thr Arg Ala Glu Pro Pro Ser Glu Pro Thr Glu Ile Arg
96 65 70 75 80
99 Pro Gln Lys Arg Lys Lys Gly Pro Ala Pro Lys Met Leu Gly Asn Glu
100 85 90 95
103 Leu Cys Ser Val Cys Gly Asp Lys Ala Ser Gly Phe His Tyr Asn Val
104 100 105 110
107 Leu Ser Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Ile Lys
108 115 120 125
111 Gly Ala His Tyr Ile Cys His Ser Gly Gly His Cys Pro Met Asp Thr
112 130 135 140
115 Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Arg Lys Cys Arg Gln
116 145 150 155 160
119 Ala Gly Met Arg Glu Glu Cys Val Leu Ser Glu Glu Gln Ile Arg Leu
120 165 170 175
123 Lys Lys Leu Lys Arg Gln Glu Glu Glu Gln Ala His Ala Thr Ser Leu
124 180 185 190
127 Pro Pro Arg Arg Ser Ser Pro Pro Gln Ile Leu Pro Gln Leu Ser Pro
128 195 200 205
131 Glu Gln Leu Gly Met Ile Glu Lys Leu Val Ala Ala Gln Gln Gln Cys
132 210 215 220
135 Asn Arg Arg Ser Phe Ser Asp Arg Leu Arg Val Thr Pro Trp Pro Met
136 225 230 235 240
139 Ala Pro Asp Pro His Ser Arg Glu Ala Arg Gln Gln Arg Phe Ala His
140 245 250 255
143 Phe Thr Glu Leu Ala Ile Val Ser Val Gln Glu Ile Val Asp Phe Ala
144 260 265 270
147 Lys Gln Leu Pro Gly Phe Leu Gln Leu Ser Arg Glu Asp Gln Ile Ala
148 275 280 285
151 Leu Leu Lys Thr Ser Ala Ile Glu Val Met Leu Leu Glu Thr Ser Arg
152 290 295 300
155 Arg Tyr Asn Pro Gly Ser Glu Ser Ile Thr Phe Leu Lys Asp Phe Ser
156 305 310 315 320
159 Tyr Asn Arg Glu Asp Phe Ala Lys Ala Gly Leu Gln Val Glu Phe Ile
160 325 330 335
163 Asn Pro Ile Phe Glu Phe Ser Arg Ala Met Asn Glu Leu Gln Leu Asn
164 340 345 350
167 Asp Ala Glu Phe Ala Leu Leu Ile Ala Ile Ser Ile Phe Ser Ala Asp
168 355 360 365
171 Arg Pro Asn Val Gln Asp Gln Leu Gln Val Glu Arg Leu Gln His Thr
172 370 375 380
175 Tyr Val Glu Ala Leu His Ala Tyr Val Ser Ile His His Pro His Asp

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176 385          390          395          400
179 Arg Leu Met Phe Pro Arg Met Leu Met Lys Leu Val Ser Leu Arg Thr
180          405          410          415
183 Leu Ser Ser Val His Ser Glu Gln Val Phe Ala Leu Arg Leu Gln Asp
184          420          425          430
187 Lys Lys Leu Pro Pro Leu Leu Ser Glu Ile Trp Asp Val His Glu
188          435          440          445
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192 <211> LENGTH: 2010
193 <212> TYPE: DNA
194 <213> ORGANISM: homo sapiens
196 <400> SEQUENCE: 3
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199 agaggaggac gaagaaaagc agagcaaggg aacccagggc aacaggagta gttcactccg      120
201 cgagaggccg tccacgagac ccccgcgcg c aggcattgagc cccgcccccc acgcattgagc      180
203 cccgcccccc gctgttgcct ggagaggggc gggacctgga gagaggctgc tccgtgaccc      240
205 caccatgtcc tctcctacca cgagttccct ggataccccc ctgacctgga atggcccccc      300
207 tcagcctggc gccccttctt cttcacccac tgtaaaggag gagggctccg agccgtggcc      360
209 cgggggtccg gaccctgatg tcccaggcac tgatgaggcc agctcagcct gcagcacaga      420
211 ctgggtcatc ccagatccc cagaggaacc agagcgcaag cgaaagaagg gccagcccc      480
213 gaagatgctg ggccacgagc tttgacctgt ctgtggggac aaggcctccg gcttccacta      540
215 caacgtgctc agctgcgaag gctgcaaggg cttcttccgg cgcagtgtgg tccgtggtgg      600
217 ggccaggcgc tatgcctgcc ggggtggcgg aacctgccag atggacgctt tcatgcggcg      660
219 caagtgccag cagtgcgggc tgcgcaagt caaggaggca gggatgaggg agcagtgcgt      720
221 cctttctgaa gaacagatcc ggaagaagaa gattcggaaa cagcagcagc aggagtca      780
223 gtcacagtcg cagtcacctg tggggccgca gggcagcagc agctcagcct ctgggcctgg      840
225 ggcttccccct ggtggatctg aggcaggcag ccagggctcc ggggaaggcg aggggtgtcc      900
227 gctaacagcg gctcaagaac taatgatcca gcagttggtg gcggcccaac tgcagtgcaa      960
229 caaacgctcc ttctccgacc agcccaaagt caccgcttgg cccctgggcg cagaccccca      1020
231 gtcccgagat gcccgccagc aacgctttgc ccacttcacg gagctggcca tcatctcagt      1080
233 ccaggagatc gtggacttcg ctaagcaagt gcctggtttc ctgcagctgg gccgggagga      1140
235 ccagatcgcc ctctgaagg catccactat cgagatcatg ctgctagaga cagccaggcg      1200
237 ctacaaccac gagacagagt gtatcacctt cttgaaggac ttcacctaca gcaaggacga      1260
239 cttccaccgt gcaggcctgc aggtggagtt catcaacccc atcttcgagt tctcgcgggc      1320
241 catgcggcgg ctgggcctgg acgacgctga gtacgacctg ctcatcgcca tcaacatctt      1380
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247 gcgcatgctc atgaagctgg tgagcctgcg cacgctgagc tctgtgcact cggagcaggt      1560
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253 agacgccggc accccttctt ctctctaggg tggaaggggc cctgggcgag cctgtagacc      1740
255 tatcggtctt catcccttgg gataagcccc agtccaggtc caggaggctc cctccctgcc      1800
257 cagcgagtct tccagaaggg gtgaaagggt tgcaggctcc gaccactgac ccttcccggc      1860
259 tgccctccct cccagctta cacctcaagc ccagcacgca gcgtaccttg aacagaggga      1920
261 ggggaggacc catggctctc cccccctagc ccgggagacc aggggccttc ctcttctctt      1980
263 gcttttattt aataaaaata aaaacagaaa
266 <210> SEQ ID NO: 4
267 <211> LENGTH: 461
268 <212> TYPE: PRT

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271 <400> SEQUENCE: 4
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277 Gly Pro Pro Gln Pro Gly Ala Pro Ser Ser Ser Pro Thr Val Lys Glu
278 20 25 30
281 Glu Gly Pro Glu Pro Trp Pro Gly Gly Pro Asp Pro Asp Val Pro Gly
282 35 40 45
285 Thr Asp Glu Ala Ser Ser Ala Cys Ser Thr Asp Trp Val Ile Pro Asp
286 50 55 60
289 Pro Glu Glu Glu Pro Glu Arg Lys Arg Lys Lys Gly Pro Ala Pro Lys
290 65 70 75 80
293 Met Leu Gly His Glu Leu Cys Arg Val Cys Gly Asp Lys Ala Ser Gly
294 85 90 95
297 Phe His Tyr Asn Val Leu Ser Cys Glu Gly Cys Lys Gly Phe Phe Arg
298 100 105 110
301 Arg Ser Val Val Arg Gly Gly Ala Arg Arg Tyr Ala Cys Arg Gly Gly
302 115 120 125
305 Gly Thr Cys Gln Met Asp Ala Phe Met Arg Arg Lys Cys Gln Gln Cys
306 130 135 140
309 Arg Leu Arg Lys Cys Lys Glu Ala Gly Met Arg Glu Gln Cys Val Leu
310 145 150 155 160
313 Ser Glu Glu Gln Ile Arg Lys Lys Lys Ile Arg Lys Gln Gln Gln Gln
314 165 170 175
317 Glu Ser Gln Ser Gln Ser Gln Ser Pro Val Gly Pro Gln Gly Ser Ser
318 180 185 190
321 Ser Ser Ala Ser Gly Pro Gly Ala Ser Pro Gly Gly Ser Glu Ala Gly
322 195 200 205
325 Ser Gln Gly Ser Gly Glu Gly Glu Gly Val Gln Leu Thr Ala Ala Gln
326 210 215 220
329 Glu Leu Met Ile Gln Gln Leu Val Ala Ala Gln Leu Gln Cys Asn Lys
330 225 230 235 240
333 Arg Ser Phe Ser Asp Gln Pro Lys Val Thr Pro Trp Pro Leu Gly Ala
334 245 250 255
337 Asp Pro Gln Ser Arg Asp Ala Arg Gln Gln Arg Phe Ala His Phe Thr
338 260 265 270
341 Glu Leu Ala Ile Ile Ser Val Gln Glu Ile Val Asp Phe Ala Lys Gln
342 275 280 285
345 Val Pro Gly Phe Leu Gln Leu Gly Arg Glu Asp Gln Ile Ala Leu Leu
346 290 295 300
349 Lys Ala Ser Thr Ile Glu Ile Met Leu Leu Glu Thr Ala Arg Arg Tyr
350 305 310 315 320
353 Asn His Glu Thr Glu Cys Ile Thr Phe Leu Lys Asp Phe Thr Tyr Ser
354 325 330 335
357 Lys Asp Asp Phe His Arg Ala Gly Leu Gln Val Glu Phe Ile Asn Pro
358 340 345 350
361 Ile Phe Glu Phe Ser Arg Ala Met Arg Arg Leu Gly Leu Asp Asp Ala
362 355 360 365
365 Glu Tyr Ala Leu Leu Ile Ala Ile Asn Ile Phe Ser Ala Asp Arg Pro

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369 Asn Val Gln Glu Pro Gly Arg Val Glu Ala Leu Gln Gln Pro Tyr Val
370 385      390      395      400
373 Glu Ala Leu Leu Ser Tyr Thr Arg Ile Lys Arg Pro Gln Asp Gln Leu
374      405      410      415
377 Arg Phe Pro Arg Met Leu Met Lys Leu Val Ser Leu Arg Thr Leu Ser
378      420      425      430
381 Ser Val His Ser Glu Gln Val Phe Ala Leu Arg Leu Gln Asp Lys Lys
382      435      440      445
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386      450      455      460
389 <210> SEQ ID NO: 5
390 <211> LENGTH: 5449
391 <212> TYPE: DNA
392 <213> ORGANISM: homo sapiens
394 <400> SEQUENCE: 5
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399 ccctcacctc ccgacgggg cgaggctcca tggctgcccc ctgcctgcac ccgtccctgg      180
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457 tcctgtgtgg ccctcctgtc tggagtgaca tcttcatctg ctctgaatac tggtgcccag      1920
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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date